AMENDMENTS TO THE CLAIMS

1. (Currently Amended) A promoter region having specificity for plant epidermis, comprising a first sequence originating from the promoter of ~~the gene~~ a GSTA1 gene and a second sequence originating from the intron of ~~the gene~~ a WIR1a gene, wherein the first sequence is SEQ ID No. 1 and the second sequence is SEQ ID No. 2 or wherein the first and/or second sequence of the promoter region have a sequence identity of at least 90% to the sequences of SEQ ID No. 1 and/or SEQ ID No. 2.

2. (Previously presented) The promoter region according to claim 1, wherein the first sequence is SEQ ID NO. 1 and the second sequence is SEQ ID No. 2.

3. (Previously presented) The promoter region according to claim 1, wherein said promoter region is selected from the group consisting of

a) promoter regions comprising the nucleic acid sequence of SEQ ID NO. 3,
b) promoter regions comprising a functional part of the nucleic acid sequence of SEQ ID NO. 3, and
c) promoter regions having a sequence which hybridizes under stringent conditions with the nucleic acid sequence of SEQ ID NO. 3.

4. (Previously presented) A chimeric gene, comprising the promoter region according to claim 1 in operative linkage with a coding sequence.

5. (Previously presented) The chimeric gene according to claim 4, wherein expression of the chimeric gene results in an increased yield of the protein encoded by the coding sequence in plant epidermis.

6. (Previously presented) The chimeric gene according to claim 4, wherein the coding sequence originates from a resistance gene.

7. (Previously presented) The chimeric gene according to claim 5, wherein the coding sequence encodes a peroxidase or an oxalate oxidase.

8. (Previously presented)The chimeric gene according to claim 4, wherein expression of the chimeric gene suppresses expression of a corresponding endogenous gene in plant epidermis.

9. (Previously presented) The chimeric gene according to claim 8, wherein the coding sequence is in antisense orientation.

10. (Previously presented) The chimeric gene according to claim 8, wherein suppression of expression of the endogenous gene results from RNA-interference.

11. (Previously presented) The chimeric gene according to claim 8, wherein the endogenous gene whose expression is suppressed is the Mlo-gene.

12. (Previously presented) A recombinant nucleic acid molecule, comprising a promoter region according to claim 1.

13. (Previously presented) The recombinant nucleic acid molecule according to claim 12, further comprising transcription termination sequences.

14. (Previously presented) A method for generating transgenic plants with epidermis specific expression of a transgene, comprising the steps:

a) generating a recombinant nucleic acid molecule according to claim 12;
b) transferring the recombinant nucleic acid molecule from a) to plant cells; and
c) regenerating entirely transformed plants and, if desired, propagating the plants.

15. (Previously presented) A transgenic plant comprising a recombinant nucleic acid molecule according to claim 12.

16. (Previously presented) The transgenic plant according to claim 15, wherein said plant is monocotyledonous plants.

17. (Previously presented) The transgenic plant according to claim 16, wherein said plant is poaceae.

18. (Previously presented) The transgenic plant according to claim 17, wherein said plant is wheat or barley.

19. (Canceled)

20. (Canceled)

21. (Previously presented) A method for increasing the pathogen resistance in transgenic plants,
comprising the steps:

a) generating a recombinant nucleic acid molecule according to claim 12,
b) transferring the recombinant nucleic acid molecule from a) to a plant cell and
c) regenerating an entirely transformed plant and, if desired, propagating said plant.

22. (Previously presented) A transgenic plant with increased pathogen resistance, containing a recombinant nucleic acid molecule according to claim 12.

23. (Previously presented) The transgenic plant according to claim 22, wherein said plant is a monocotyledonous plant.

24. (Previously presented) The transgenic plant according to claim 23, wherein said plant is poaceae.

25. (Previously presented) The transgenic plant according to claim 24, wherein said plant is wheat or barley.

26. (Previously presented) The transgenic plant according to claim 22, wherein the plant exhibits an increased resistance against mildew.

27. (Previously presented) A transgenic part of a transgenic plant comprising a recombinant nucleic acid molecule according to claim 12 and transgenic propagation material.

28. (Previously presented) The transgenic part of claim 27, wherein the transgenic part is selected from the group consisting of protoplasts, plant cells, calli, seeds, tubers and cuttings.

29. (Previously presented) A transgenic offspring of a transgenic plant comprising a recombinant nucleic acid molecule according to claim 12.

30. (Previously presented) A transgenic part of a transgenic plant with increased pathogen resistance, generated according to the method of claim 21, and transgenic propagation material.

31. (Previously presented) The transgenic part of claim 30, wherein the transgenic part is selected from the group consisting of protoplasts, plant cells, calli, seeds, tubers and cuttings.

32. (Previously presented) A transgenic offspring of a transgenic plant with increased pathogen resistance, generated according to the method of claim 21.

33. (New) The promoter region according to claim 1, wherein the first sequence is SEQ ID No. 1 and the second sequence is SEQ ID No. 2 or wherein the first and/or second sequence of the promoter region have a sequence identity of at least 95% to the sequences of SEQ ID No. 1 and/or SEQ ID No. 2.

34. (New) A promoter region having specificity for plant epidermis, comprising a first sequence originating from the promoter of the gene GSTA1 and a second sequence originating from the intron of the gene WIR1a, wherein the first sequence is SEQ ID No. 1 and the second sequence is SEQ ID No. 2 or wherein the first and/or second sequence of the promoter region hybridize under stringent conditions to the sequences of SEQ ID No. 1 and/or SEQ ID No. 2.